

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Stern, David M.
Yan, Shi Du
- (ii) TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
NEURODEGENERATIVE CONDITIONS
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: U.S.A.
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/815,225
(B) FILING DATE: 12-MAR-1997
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 0575/55209
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 278-0400
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS

(B) LOCATION: 19..801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAGTGGCCG GCGACAAG	ATG GCA GCA GCG TGT CGG AGC GTG AAG GGC CTG	51
	Met Ala Ala Ala Cys Arg Ser Val Lys Gly Leu	
	1 5 10	
GTG GCG GTA ATA ACC GGA GGA GCC TCG GGC CTG GGC CTG GCC ACG GCG	99	
Val Ala Val Ile Thr Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala		
	15 20 25	
GAG CGA CTT GTG GGG CAG GGA GCC TCT GCT GTG CTT CTG GAC CTG CCC	147	
Glu Arg Leu Val Gly Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro		
	30 35 40	
AAC TCG GGT GGG GAG GCC CAA GCC AAG AAG TTA GGA AAC AAC TGC GTT	195	
Asn Ser Gly Gly Glu Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val		
	45 50 55	
TTC GCC CCA GCC GAC GTG ACC TCT GAG AAG GAT GTG CAA ACA GCT CTG	243	
Phe Ala Pro Ala Asp Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu		
	60 65 70 75	
GCT CTA GCA AAA GGA AAG TTT GGC CGT GTG GAT GTA GCT GTC AAC TGT	291	
Ala Leu Ala Lys Gly Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys		
	80 85 90	
GCA GGC ATC GCG GTG GCT AGC AAG ACG TAC AAC TTA AAG AAG GGC CAG	339	
Ala Gly Ile Ala Val Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln		
	95 100 105	
ACC CAT ACC TTG GAA GAC TTC CAG CGA GTT CTT GAT GTG AAT CTC ATG	387	
Thr His Thr Leu Glu Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met		
	110 115 120	
GGC ACC TTC AAT GTG ATC CGC CTG GTG GCT GGT GAG ATG GGC CAG AAT	435	
Gly Thr Phe Asn Val Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn		
	125 130 135	
GAA CCA GAC CAG GGA GGC CAA CGT GGG GTC ATC ATC AAC ACT GCC AGT	483	
Glu Pro Asp Gln Gly Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser		
	140 145 150 155	
GTG GCT GCC TTC GAG GGT CAG GTT GGA CAA GCT GCA TAC TCT GCT TCC	531	
Val Ala Ala Phe Glu Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser		
	160 165 170	
AAG GGG GGA ATA GTG GGC ATG ACA CTG CCC ATT GCT CGG GAT CTG GCT	579	
Lys Gly Gly Ile Val Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala		
	175 180 185	
CCC ATA GGT ATC CGG GTG ATG ACC ATT GCC CCA GGT CTG TTT GGC ACC	627	
Pro Ile Gly Ile Arg Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr		
	190 195 200	

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CCA CTG CTG ACC AGC CTC CCA GAG AAA GTG TGC AAC TTC TTG GCC AGC	675
Pro Leu Leu Thr Ser Leu Pro Glu Lys Val Cys Asn Phe Leu Ala Ser	
205 210 215	
CAA GTG CCC TTC CCT AGC CGA CTG GGT GAC CCT GCT GAG TAT GCT CAC	723
Gln Val Pro Phe Pro Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His	
220 225 230 235	
CTC GTA CAG GCC ATC ATC GAG AAC CCA TTC CTC AAT GGA GAG GTC ATC	771
Leu Val Gln Ala Ile Ile Glu Asn Pro Phe Leu Asn Gly Glu Val Ile	
240 245 250	
CGG CTG GAT GGG GCC ATT CGT ATG CAG CCT TGAAGGGAGA AGGCAGAGAA	821
Arg Leu Asp Gly Ala Ile Arg Met Gln Pro	
255 260	
AACACACGCT CCTCTGCCCT TCCTTTCCCT GGGGTACTAC TCTCCAGCTT GGGAGGAAGC	881
CCAGTAGCCA TTTTGTAACCT GCCTACCACT CGCCCTCTGT GCCTAATAAA GTCTCTTTTT	941
CTCACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	981

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Ala Cys Arg Ser Val Lys Gly Leu Val Ala Val Ile Thr
1 5 10 15

Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Glu Arg Leu Val Gly
20 25 30

Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu
35 40 45

Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp
50 55 60

Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
65 70 75 80

Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
85 90 95

Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
100 105 110

Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val

115		120		125
Ile Arg Leu Val Ala Gly	Glu Met Gly Gln Asn Glu Pro Asp Gln Gly			
130	135	140		
Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu				
145	150	155		160
Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val				
	165	170		175
Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg				
	180	185		190
Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser				
	195	200		205
Leu Pro Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro				
	210	215		220
Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile				
225	230	235		240
Ile Glu Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala				
	245	250		255
Ile Arg Met Gln Pro				
	260			

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Ala Ala Cys Arg Ser Val Lys Gly Leu Val Ala Val Ile Thr	
1	5 10 15
Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Glu Arg Leu Val Gly	
	20 25 30
Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu	
	35 40 45
Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp	
	50 55 60

Val	Thr	Ser	Glu	Lys	Asp	Val	Gln	Thr	Ala	Leu	Ala	Leu	Ala	Lys	Gly	65	70	75	80
Lys	Phe	Gly	Arg	Val	Asp	Val	Ala	Val	Asn	Cys	Ala	Gly	Ile	Ala	Val	85	90	95	
Ala	Ser	Lys	Thr	Tyr	Asn	Leu	Lys	Lys	Gly	Gln	Thr	His	Thr	Leu	Glu	100	105	110	
Asp	Phe	Gln	Arg	Val	Leu	Asp	Val	Asn	Leu	Met	Gly	Thr	Phe	Asn	Val	115	120	125	
Ile	Arg	Leu	Val	Ala	Gly	Glu	Met	Gly	Gln	Asn	Glu	Pro	Asp	Gln	Gly	130	135	140	
Gly	Gln	Arg	Gly	Val	Ile	Ile	Asn	Thr	Ala	Ser	Val	Ala	Ala	Phe	Glu	145	150	155	160
Gly	Gln	Val	Gly	Gln	Ala	Ala	Tyr	Ser	Ala	Ser	Lys	Gly	Gly	Ile	Val	165	170	175	
Gly	Met	Thr	Leu	Pro	Ile	Ala	Arg	Asp	Leu	Ala	Pro	Ile	Gly	Ile	Arg	180	185	190	
Val	Met	Thr	Ile	Ala	Pro	Gly	Leu	Phe	Gly	Thr	Pro	Leu	Leu	Thr	Ser	195	200	205	
Leu	Pro	Glu	Lys	Val	Cys	Asn	Phe	Leu	Ala	Ser	Gln	Val	Pro	Phe	Pro	210	215	220	
Ser	Arg	Leu	Gly	Asp	Pro	Ala	Glu	Tyr	Ala	His	Leu	Val	Gln	Ala	Ile	225	230	235	240
Ile	Glu	Asn	Pro	Phe	Leu	Asn	Gly	Glu	Val	Ile	Arg	Leu	Asp	Gly	Ala	245	250	255	
Ile	Arg	Met	Gln	Pro												260			

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asn	Asp	Leu	Ser	Gly	Lys	Thr	Val	Ile	Ile	Thr	Gly	Gly	Ala	Arg	1	5	10	15
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Gly	Leu	Gly	Ala	Glu	Ala	Ala	Arg	Gln	Ala	Val	Ala	Ala	Gly	Ala	Arg	20	25	30
Val	Val	Leu	Ala	Asp	Val	Leu	Asp	Glu	Glu	Gly	Ala	Ala	Thr	Ala	Arg	35	40	45
Glu	Leu	Gly	Asp	Ala	Ala	Arg	Tyr	Gln	His	Leu	Asp	Val	Thr	Ile	Glu	50	55	60
Glu	Asp	Trp	Gln	Arg	Val	Val	Ala	Tyr	Ala	Arg	Glu	Glu	Phe	Gly	Ser	65	70	75
Val	Asp	Gly	Leu	Val	Asn	Asn	Ala	Gly	Ile	Ser	Thr	Gly	Met	Phe	Leu	85	90	95
Glu	Thr	Glu	Ser	Val	Glu	Arg	Phe	Arg	Lys	Val	Val	Asp	Ile	Asn	Leu	100	105	110
Thr	Gly	Val	Phe	Ile	Gly	Met	Lys	Thr	Val	Ile	Pro	Ala	Met	Lys	Asp	115	120	125
Ala	Gly	Gly	Gly	Ser	Ile	Val	Asn	Ile	Ser	Ser	Ala	Ala	Gly	Leu	Met	130	135	140
Gly	Leu	Ala	Leu	Thr	Ser	Ser	Tyr	Gly	Ala	Ser	Lys	Trp	Gly	Val	Arg	145	150	155
Gly	Leu	Ser	Lys	Leu	Ala	Ala	Val	Glu	Leu	Gly	Thr	Asp	Arg	Ile	Arg	165	170	175
Val	Asn	Ser	Val	His	Pro	Gly	Met	Thr	Tyr	Thr	Pro	Met	Thr	Ala	Glu	180	185	190
Thr	Gly	Ile	Arg	Gln	Gly	Glu	Gly	Asn	Tyr	Pro	Asn	Thr	Pro	Met	Gly	195	200	205
Arg	Val	Gly	Asn	Glu	Pro	Gly	Glu	Ile	Ala	Gly	Ala	Val	Val	Lys	Leu	210	215	220
Leu	Ser	Asp	Thr	Ser	Ser	Tyr	Val	Thr	Gly	Ala	Glu	Leu	Ala	Val	Asp	225	230	235
Gly	Gly	Trp	Thr	Thr	Gly	Pro	Thr	Val	Lys	Tyr	Val	Met	Gly	Gln		245	250	255

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Gly Asp Ser

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